

SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 11:26:05 ; Search time 9284 Seconds
(without alignments)
11115.873 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgaggggtga.....ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

Regular search
w/SEQ ID NO:1

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%		Query		DB	ID	Description
No.	Score	Match	Length	Length	Score			
1	2381	100.0	2381	6	AX404864	WO 02/26787	AX404864	Sequence
2	2377.8	99.9	333150	1	AP005277	2002 GenBank	AP005277	Corynebac
3	2377.8	99.9	349980	6	AX127146	EP1108790	AX127146	Sequence
4	2377.8	99.9	349980	6	AX127147	EP	AX127147	Sequence
5	2156.8	90.6	2326	6	AX764083	WO 03/40289	AX764083	Sequence
6	2126.8	89.3	2196	6	AX121362	EP	AX121362	Sequence
7	2126.8	89.3	2196	6	BD163479	JF2002191370	BD163479	Novel pol
8	1498.4	62.9	308650	1	AP005218		AP005218	Corynebac
9	1039	43.6	347625	1	BX248356		BX248356	Corynebac
10	590.6	24.8	11785	1	AE012833		AE012833	Chlorobi
c 11	583.6	24.5	12009	1	AE011922		AE011922	Xanthomon
c 12	574.2	24.1	10101	1	AE012376		AE012376	Xanthomon
13	563.8	23.7	17916	1	AE007004		AE007004	Mycobacte
14	563.8	23.7	75216	6	AX704275		AX704275	Sequence
15	563.8	23.7	348264	1	BX842576		BX842576	Mycobacte
16	562.2	23.6	299450	1	BX248338		BX248338	Mycobacte
17	545	22.9	2333	1	KPNDEAD		L08387	Klebsiella
c 18	519.8	21.8	300029	1	AE012553		AE012553	Xylella f
c 19	519.6	21.8	12008	1	AE003878		AE003878	Xylella f
c 20	516	21.7	11002	1	AE015331		AE015331	Shigella
c 21	516	21.7	292497	1	AE016989		AE016989	Shigella
c 22	516	21.7	300359	1	AE016767		AE016767	Escherich
c 23	514.6	21.6	14820	1	AE000397		AE000397	Escherich
c 24	514.6	21.6	14820	6	AX370215		AX370215	Sequence
c 25	514.6	21.6	14820	6	AX370260		AX370260	Sequence
c 26	514.6	21.6	110000	1	ECOUW67_0		U18997	Escherichia
c 27	513.6	21.6	110000	2	AC074221_3			Continuation (4 of
c 28	511.4	21.5	20120	1	AE008851		AE008851	Salmonell
c 29	508	21.3	10994	1	AE005544		AE005544	Escherich
c 30	508	21.3	307962	1	AP002564		AP002564	Escherich
31	500.8	21.0	2863	6	BD103627		BD103627	Method an
c 32	500.2	21.0	258050	1	AL627278		AL627278	Salmonell
c 33	500.2	21.0	301574	1	AE016844		AE016844	Salmonell

App'l's WO

Pompejus

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 11:24:21 ; Search time 973 Seconds
(without alignments)
10395.642 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgaggggtga.....ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	2381	100.0	2381	6	AAD28043	Aad28043 Corynebac
2	2377.8	99.9	349980	5	AAH68527	Aah68527 C glutami
3	2377.8	99.9	349980	5	AAH68528	Aah68528 C glutami
4	2126.8	89.3	2196	5	AAH66243	Aah66243 C glutami
5	1674	70.3	1674	7	ACA00444	Aca00444 C. glutam
6	997.2	41.9	1694	7	ACA29908	Aca29908 Prokaryot
7	614.8	25.8	1698	7	ACA37563	Aca37563 Prokaryot

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:22:26 ; Search time 195 Seconds
(without alignments)
6776.093 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		ID	Description
	No.	Score	Match	Length	DB			
	1	563.8	23.7	4403765	3	US-09-103-840A-2		Sequence 2, Appli
	2	563.8	23.7	4411529	3	US-09-103-840A-1		Sequence 1, Appli
	3	500.8	21.0	2863	4	US-09-293-427-5		Sequence 5, Appli
	4	475.2	20.0	1455	4	US-09-489-039A-6537		Sequence 6537, Ap
	5	465.4	19.5	2100	4	US-09-252-991A-9660		Sequence 9660, Ap
	6	465.2	19.5	1785	4	US-09-252-991A-9701		Sequence 9701, Ap
c	7	403.6	17.0	1329	4	US-09-489-039A-6439		Sequence 6439, Ap
	8	373	15.7	1851	4	US-09-543-681A-1595		Sequence 1595, Ap
	9	357.6	15.0	1830121	4	US-09-557-884-1		Sequence 1, Appli
	10	357.6	15.0	1830121	4	US-09-643-990A-1		Sequence 1, Appli
c	11	295.8	12.4	640681	4	US-09-790-988-1		Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 17:44:52 ; Search time 1060 Seconds
(without alignments)
10208.487 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2953838 seqs, 2272363821 residues

Total number of hits satisfying chosen parameters: 5907676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Nakagawa
USPAP 2002
0197605

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2381	100.0	2381	9	US-09-963-790A-1	Sequence 1, Appli
2	2377.8	99.9	3309400	9	US-09-738-626-1	Sequence 1, Appli
3	2126.8	89.3	2196	9	US-09-738-626-1278	Sequence 1278, Ap
4	997.2	41.9	1694	13	US-10-282-122A-17778	Sequence 17778, A
5	614.8	25.8	1698	13	US-10-282-122A-25433	Sequence 25433, A
6	577.4	24.3	1515	16	US-10-369-493-39349	Sequence 39349, A
7	577.4	24.3	1515	16	US-10-369-493-39740	Sequence 39740, A
8	572.6	24.0	1392	16	US-10-369-493-38983	Sequence 38983, A
9	563.8	23.7	1692	13	US-10-282-122A-28332	Sequence 28332, A
10	563.8	23.7	75216	15	US-10-080-170-646	Sequence 646, App
11	562.2	23.6	1689	13	US-10-282-122A-26634	Sequence 26634, A
12	545	22.9	1929	13	US-10-282-122A-23307	Sequence 23307, A
13	540	22.7	1893	13	US-10-282-122A-20013	Sequence 20013, A
14	523	22.0	1695	16	US-10-369-493-32859	Sequence 32859, A
15	521	21.9	1737	16	US-10-369-493-33102	Sequence 33102, A
16	519.6	21.8	1845	16	US-10-369-493-41191	Sequence 41191, A
17	514.6	21.6	1941	9	US-09-815-242-6214	Sequence 6214, Ap
18	514.6	21.6	1941	13	US-10-282-122A-7172	Sequence 7172, Ap
19	500.2	21.0	1941	9	US-09-815-242-9671	Sequence 9671, Ap
20	500.2	21.0	1941	13	US-10-282-122A-39344	Sequence 39344, A
21	488.8	20.5	1920	16	US-10-369-493-24059	Sequence 24059, A
22	469	19.7	1647	16	US-10-369-493-44595	Sequence 44595, A
23	468.4	19.7	1704	9	US-09-815-242-7788	Sequence 7788, Ap
24	468.4	19.7	1704	13	US-10-282-122A-30236	Sequence 30236, A
25	448.8	18.8	1726	13	US-10-282-122A-33397	Sequence 33397, A
26	446.8	18.8	1708	16	US-10-369-493-37429	Sequence 37429, A
27	445.4	18.7	1714	13	US-10-282-122A-31439	Sequence 31439, A
28	443.2	18.6	1995	13	US-10-282-122A-41749	Sequence 41749, A
29	398.6	16.7	1415	13	US-10-282-122A-36654	Sequence 36654, A
30	367.8	15.4	1833	13	US-10-282-122A-32588	Sequence 32588, A
31	357.6	15.0	1842	9	US-09-815-242-6893	Sequence 6893, Ap
32	357.6	15.0	1842	13	US-10-282-122A-21926	Sequence 21926, A
33	357.6	15.0	1830121	15	US-10-329-960-1	Sequence 1, Appli
34	357.6	15.0	1830121	16	US-10-329-670-1	Sequence 1, Appli
35	355.6	14.9	1992	13	US-10-282-122A-41471	Sequence 41471, A
36	347.6	14.6	1833	13	US-10-282-122A-31003	Sequence 31003, A
37	347.6	14.6	1833	13	US-10-406-686A-87	Sequence 87, Appl
38	337.2	14.2	1337	16	US-10-369-493-42992	Sequence 42992, A
39	328.2	13.8	1620	16	US-10-369-493-31859	Sequence 31859, A
40	326	13.7	1767	13	US-10-282-122A-25322	Sequence 25322, A
41	324.4	13.6	1701	16	US-10-369-493-32830	Sequence 32830, A
c 42	295.8	12.4	640681	9	US-09-790-988-1	Sequence 1, Appli
43	284.4	11.9	1722	13	US-10-282-122A-14689	Sequence 14689, A
44	280.8	11.8	1431	16	US-10-369-493-40518	Sequence 40518, A
45	278.4	11.7	1377	16	US-10-369-493-44540	Sequence 44540, A

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:30:16 ; Search time 6138 Seconds
(without alignments)
11583.879 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgaggtga.....ctctctagtcagagtgcgag 2381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	346.8	14.6	1231	29	CG748798		CG748798	P042-4-C0
c	2	324.4	13.6	1269	29	CG747958		CG747958	P041-3-G1
c	3	241	10.1	3539	28	BH770982		BH770982	LLMGtag70
	4	213.2	9.0	1101	28	BZ549647		BZ549647	pacs1-60
	5	195.4	8.2	1443	12	BM321064		BM321064	rockefell
	6	193.6	8.1	1929	11	AY104966		AY104966	Zea mays
c	7	190.6	8.0	936	28	BZ566692		BZ566692	pacs2-164
	8	190	8.0	1175	14	CD508153		CD508153	CDA89-C04
c	9	183.4	7.7	712	28	BZ549701		BZ549701	pacs1-60
	10	181.8	7.6	948	28	BZ553880		BZ553880	pacs1-60
	11	180.2	7.6	1609	11	AY109160		AY109160	Zea mays
	12	177.2	7.4	1772	11	AK077429		AK077429	Mus muscu
	13	172.8	7.3	1393	11	BC032078		BC032078	Homo sapi
	14	172.4	7.2	1793	11	BC012282		BC012282	Mus muscu
	15	172	7.2	1748	11	AK076982		AK076982	Mus muscu
	16	172	7.2	1752	11	AK010310		AK010310	Mus muscu
	17	167.4	7.0	544	28	AQ989915		AQ989915	Rfc00591
	18	167	7.0	1418	11	AK010644		AK010644	Mus muscu
	19	167	7.0	1438	11	AK075920		AK075920	Mus muscu
	20	163.6	6.9	1165	14	CD507904		CD507904	CDA87-G05
	21	163.6	6.9	1201	9	AL568646		AL568646	AL568646
	22	159.8	6.7	935	14	CF651366		CF651366	29-E00921
	23	158.2	6.6	1050	29	AY414350		AY414350	Mus muscu
	24	157	6.6	688	14	CF842193		CF842193	psHB018xI
c	25	156.8	6.6	696	28	BH143507		BH143507	TDGEA79TH
	26	156.4	6.6	907	14	CK263230		CK263230	EST709308
	27	155.6	6.5	786	28	BZ564147		BZ564147	pacs2-164
	28	155.6	6.5	802	13	BU476989		BU476989	603841415
	29	155.2	6.5	972	11	CNS08PRP		BX022817	Single re
	30	153	6.4	1031	11	CNS08DJ2		BX006954	Single re
	31	152.6	6.4	835	28	BZ565507		BZ565507	pacs2-164
	32	152.4	6.4	1091	14	CK206257		CK206257	FGAS01784
	33	152	6.4	1012	13	BU112303		BU112303	603129440
	34	151.2	6.4	1059	29	AY404229		AY404229	Homo sapi
	35	150	6.3	694	14	CF886658		CF886658	tric084xc
	36	150	6.3	748	14	CB907999		CB907999	tric084xc
	37	149.4	6.3	1163	14	CD497898		CD497898	CDA30-E05
	38	148.2	6.2	1201	9	AL535247		AL535247	AL535247
	39	148.2	6.2	2972	11	AK031534		AK031534	Mus muscu
	40	147.6	6.2	871	14	CD439282		CD439282	EL01N0523
	41	147	6.2	1033	11	CNS090JP		BX036785	Single re
	42	146.6	6.2	2986	11	AK028274		AK028274	Mus muscu
	43	146.6	6.2	3956	11	BC043699		BC043699	Mus muscu
	44	146.4	6.1	1629	11	AK076509		AK076509	Mus muscu
	45	145.8	6.1	704	13	BU406237		BU406237	603482292

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 19:30:42 ; Search time 9282 Seconds
(without alignments)
11118.268 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaacccgcaggggtga.....ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

OLIGO Search
w/SEQ ID NO:1

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2381	100.0	2381	6	AX404864	Sequence
2	2279	95.7	333150	1	AP005277	Corynebac
3	2279	95.7	349980	6	AX127146	Sequence
4	2279	95.7	349980	6	AX127147	Sequence
5	2058	86.4	2326	6	AX764083	Sequence
6	2028	85.2	2196	6	AX121362	Sequence
7	2028	85.2	2196	6	BD163479	Novel pol
8	44	1.8	308650	1	AP005218	Corynebac
c 9	26	1.1	10101	1	AE012376	Xanthomon
10	26	1.1	123385	1	BX640452	Bordetell
11	26	1.1	255260	1	BX640436	Bordetell
12	26	1.1	346359	1	BX640411	Bordetell
c 13	26	1.1	347356	1	BX640437	Bordetell
14	26	1.1	347625	1	BX248356	Corynebac
15	26	1.1	348134	1	BX640420	Bordetell
c 16	26	1.1	348251	1	BX640423	Bordetell
17	24	1.0	12514	1	AE012011	Xanthomon
c 18	24	1.0	320150	1	AP005033	Streptomy
19	23	1.0	10491	1	AE005859	Caulobact
c 20	23	1.0	12039	1	AE009534	Brucella
21	23	1.0	12080	1	AE014406	Brucella
c 22	23	1.0	109911	2	AC118330_4	Continuation (5 of
23	23	1.0	190050	1	AL646059	Ralstonia
c 24	23	1.0	198050	1	AL646061	Ralstonia
c 25	23	1.0	217794	2	AC111124	Mus muscu
26	23	1.0	237801	2	AC137306	Rattus no
c 27	23	1.0	238039	2	AC137290	Rattus no
c 28	23	1.0	300750	1	AP006576	Gloeobact
29	23	1.0	301617	1	AE016911	Chromobac
30	23	1.0	305584	1	AE016920	Chromobac
c 31	23	1.0	311000	1	SCO939122	Streptomy
32	23	1.0	311583	2	AC105794	Rattus no
33	23	1.0	347660	1	AP002994	Mesorhizo

W002/26787

2002 GenBank

EP1108790

EP

W003/40289

EP

JP2002191370

2002

GenBank

AP005218

Bompejus

efficiens

diphtheriae

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 17:48:26 ; Search time 974 Seconds
(without alignments)
10384.969 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgaggggtga.....ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2381	100.0	2381	6	AAD28043	Aad28043 Corynebac
2	2279	95.7	349980	5	AAH68527	Aah68527 C glutami
3	2279	95.7	349980	5	AAH68528	Aah68528 C glutami
4	2028	85.2	2196	5	AAH66243	Aah66243 C glutami
5	1674	70.3	1674	7	ACA00444	Aca00444 C. glutam
6	184	7.7	273	7	ACA00443	Aca00443 C. glutam
7	26	1.1	1694	7	ACA29908	Aca29908 Prokaryot

WD 02/26787

EP 1108790

EP

EP

EP

WD 02/77183

DE 10128510 (2001)

PR June

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 21:48:17 ; Search time 193 Seconds
(without alignments)
6846.311 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgaggggtga.....ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description	
	Query	Match	Length	DB	ID		
No.	Score						
c	1	20	0.8	483	4	US-09-252-991A-5687	Sequence 5687, Ap
	2	20	0.8	1284	4	US-09-489-039A-841	Sequence 841, App
	3	20	0.8	2328	4	US-09-252-991A-5729	Sequence 5729, Ap
	4	20	0.8	2863	4	US-09-293-427-5	Sequence 5, Appli
c	5	20	0.8	4230	4	US-09-252-991A-5711	Sequence 5711, Ap
	6	20	0.8	4941	4	US-09-252-991A-5741	Sequence 5741, Ap
	7	20	0.8	68750	3	US-09-335-409-1	Sequence 1, Appli
	8	20	0.8	68750	4	US-09-568-102-1	Sequence 1, Appli
	9	20	0.8	68750	4	US-09-567-969-1	Sequence 1, Appli
	10	20	0.8	68750	4	US-09-568-480-1	Sequence 1, Appli
	11	20	0.8	68750	4	US-09-568-486-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 22:22:22 ; Search time 1947 Seconds
(without alignments)
5562.883 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgagggtga.....ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query		Length	DB	ID	Description
	No.	Score Match				
	1	2381 100.0	2381	9	US-09-963-790A-1	Sequence 1, Appli
	2	2279 95.7	3309400	9	US-09-738-626-1	Sequence 1, Appli
	3	2028 85.2	2196	9	US-09-738-626-1278	Sequence 1278, Ap
	4	26 1.1	1392	16	US-10-369-493-38983	Sequence 38983, A
	5	26 1.1	1515	16	US-10-369-493-39349	Sequence 39349, A
	6	26 1.1	1515	16	US-10-369-493-39740	Sequence 39740, A
	7	26 1.1	1694	13	US-10-282-122A-17778	Sequence 17778, A
	8	26 1.1	1722	13	US-10-282-122A-14689	Sequence 14689, A
	9	25 1.0	1708	16	US-10-369-493-37429	Sequence 37429, A
	10	24 1.0	2064	15	US-10-156-761-2902	Sequence 2902, Ap
	11	24 1.0	125746	15	US-10-156-761-15102	Sequence 15102, A
c	12	24 1.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
	13	23 1.0	1326	16	US-10-369-493-41631	Sequence 41631, A
	14	23 1.0	1404	16	US-10-369-493-35503	Sequence 35503, A
	15	23 1.0	1554	16	US-10-369-493-40612	Sequence 40612, A
	16	23 1.0	1584	16	US-10-369-493-35498	Sequence 35498, A
	17	22 0.9	198	11	US-09-864-408A-6929	Sequence 6929, Ap
	18	22 0.9	603	15	US-10-156-761-1568	Sequence 1568, Ap
c	19	22 0.9	2742	13	US-10-282-122A-17561	Sequence 17561, A
	20	21 0.9	28	9	US-09-963-790A-3	Sequence 3, Appli
c	21	21 0.9	28	9	US-09-963-790A-4	Sequence 4, Appli
	22	21 0.9	600	16	US-10-369-493-41629	Sequence 41629, A
c	23	20 0.8	503	10	US-09-918-995-34274	Sequence 34274, A
	24	20 0.8	1266	9	US-09-815-242-7606	Sequence 7606, Ap
	25	20 0.8	1335	16	US-10-369-493-35231	Sequence 35231, A
	26	20 0.8	1387	16	US-10-369-493-35268	Sequence 35268, A
c	27	20 0.8	1584	15	US-10-270-333-140	Sequence 140, App
	28	20 0.8	1941	9	US-09-815-242-6214	Sequence 6214, Ap
	29	20 0.8	1941	13	US-10-282-122A-7172	Sequence 7172, Ap
	30	20 0.8	4185	15	US-10-270-333-139	Sequence 139, App
	31	20 0.8	68750	14	US-10-014-717-1	Sequence 1, Appli
	32	20 0.8	71989	13	US-09-727-889-2	Sequence 2, Appli
c	33	20 0.8	203070	13	US-10-087-192-247	Sequence 247, App
	34	19 0.8	480	9	US-09-991-496-132	Sequence 132, App
	35	19 0.8	515	9	US-09-917-800A-583	Sequence 583, App
c	36	19 0.8	520	9	US-09-874-923-29	Sequence 29, Appl
c	37	19 0.8	520	9	US-09-991-496-29	Sequence 29, Appl
	38	19 0.8	522	15	US-10-156-761-2688	Sequence 2688, Ap
	39	19 0.8	528	13	US-10-424-599-47907	Sequence 47907, A
	40	19 0.8	546	15	US-10-156-761-1619	Sequence 1619, Ap
	41	19 0.8	557	9	US-09-917-800A-340	Sequence 340, App
	42	19 0.8	561	15	US-10-156-761-3799	Sequence 3799, Ap
	43	19 0.8	871	13	US-10-424-599-9675	Sequence 9675, Ap
	44	19 0.8	1098	13	US-10-389-647-129	Sequence 129, App
c	45	19 0.8	1137	15	US-10-156-761-6123	Sequence 6123, Ap

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 21:41:22 ; Search time 6139 Seconds
(without alignments)
11581.992 Million cell updates/sec

Title: US-09-963-790A-1
Perfect score: 2381
Sequence: 1 caggaaaccccgaggggtga.....ctctctagtcagagtgcgag 2381

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.		%					
1	23	1.0	413	14	CK233812	CK233812	re20a03.y
2	23	1.0	604	14	CF980889	CF980889	re10b06.y
3	22	0.9	471	9	AU284741	AU284741	AU284741
4	22	0.9	478	14	CF075999	CF075999	Hd_mx17_6
5	22	0.9	562	12	BJ411196	BJ411196	BJ411196
6	22	0.9	631	9	AU268561	AU268561	AU268561
c 7	22	0.9	660	12	BM634053	BM634053	170006688
c 8	22	0.9	714	12	BM656204	BM656204	170006873
c 9	21	0.9	573	13	BU543982	BU543982	GM880001A
10	21	0.9	575	28	BZ345001	BZ345001	hr43d08.b
11	21	0.9	606	12	BM603218	BM603218	170006870
12	21	0.9	612	28	AZ418854	AZ418854	1M0195C09
13	21	0.9	715	13	BU634805	BU634805	018D02 In
14	21	0.9	848	10	BF260369	BF260369	HVSMEf002
c 15	20	0.8	160	28	AZ921472	AZ921472	1006030B0
16	20	0.8	261	14	CD942465	CD942465	RBX_51 Ge
17	20	0.8	262	14	CD947789	CD947789	SAB_30 Ge
18	20	0.8	262	14	CD950568	CD950568	SAR_125 G
19	20	0.8	262	14	CD951995	CD951995	SAZ_86 Ge
20	20	0.8	263	14	CD948209	CD948209	SAD_64 Ge
c 21	20	0.8	275	12	BI674592	BI674592	949022D11
22	20	0.8	305	9	AA571940	AA571940	vg12d02.r
c 23	20	0.8	327	28	BH228484	BH228484	1006147C0
c 24	20	0.8	330	28	BH228575	BH228575	1006147F0
c 25	20	0.8	340	28	BH217878	BH217878	1006060G0
26	20	0.8	344	13	BQ760997	BQ760997	EBro04 SQ
c 27	20	0.8	344	28	BH216414	BH216414	1006042E0
c 28	20	0.8	351	28	BH217881	BH217881	1006060G0
c 29	20	0.8	352	28	AZ921694	AZ921694	1006031E0
c 30	20	0.8	352	28	BH216419	BH216419	1006042E0
c 31	20	0.8	352	28	BH228573	BH228573	1006147F0
c 32	20	0.8	353	28	BH228482	BH228482	1006147C0
c 33	20	0.8	355	28	BH228632	BH228632	1006147H0
34	20	0.8	363	13	BQ993892	BQ993892	QGF5M01.y
35	20	0.8	383	10	AW417369	AW417369	53455 MAR
36	20	0.8	385	10	AW115311	AW115311	rs65e07.y
37	20	0.8	393	10	AW307746	AW307746	1617 MARC
c 38	20	0.8	399	14	CF629810	CF629810	zmrws48_0
39	20	0.8	404	14	CD947936	CD947936	SAC_212 G
40	20	0.8	410	12	BI336407	BI336407	AR095H07S
41	20	0.8	462	14	CF215031	CF215031	CAST0001_
c 42	20	0.8	471	14	CF215115	CF215115	CAST0001_
c 43	20	0.8	472	29	CG340791	CG340791	OGVCR31TH
44	20	0.8	482	10	BE481452	BE481452	166898 BA
45	20	0.8	484	12	BM106031	BM106031	509650 MA